

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 26, 2002, 20:33:06 : Search time 1798 Seconds
(without alignments)
8065.678 Million cell updates/sec

Title: US-09-840-795-18_COPY_78_770

Perfect score: 693
Sequence: 1 atgagatgcgaagaataatga.....agcagcaggggcctgaatg 693

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Genemdb1:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
------------	-------------	-------	--------	----	-------------

1	611.4	88.2	1162	6	AX127536	AX127536 Sequence
2	609.4	87.9	894	6	AF298812	AF298812 Homo sapi
3	446.6	64.4	891	6	AX127563	AX127563 Sequence
4	446.4	64.4	807	6	AX127538	AX127538 Sequence
5	413.2	59.6	1081	6	AX127585	AX127585 Sequence
6	393.2	56.7	534	6	AX127556	AX127556 Sequence
7	393.2	56.7	1200	6	AX127557	AX127557 Sequence
8	317.4	45.8	801	6	AX127565	AX127565 Sequence
9	315.4	45.5	519	6	AX127574	AX127574 Sequence
10	257	37.1	528	6	AX127568	AX127568 Sequence
11	220.4	31.8	529	6	AX127566	AX127566 Sequence
12	181.4	26.2	192505	6	AL353136	AL353136 Human DNA
13	181.4	26.2	205736	2	AC023560	AC023560 Homo sapi
14	163.2	23.5	744	10	AB040433	AB040433 Mus muscu
15	163.2	23.5	886	10	AF167553	AF167553 Mus muscu
16	163.2	23.5	1075	10	AF173166	AF173166 Mus muscu
17	163.2	23.5	1678	10	AF167552	AF167552 Mus muscu
18	163.2	23.5	1914	6	AX213199	AX213199 Sequence
19	163.2	23.5	1914	10	AF247000	AF247000 Mus muscu
20	163.2	23.5	3964	10	AB040432	AB040432 Mus muscu
21	156.4	22.6	1489	9	AF167555	AF167555 Homo sapi
22	154.8	22.3	1254	6	AX151748	AX151748 Sequence
23	154.8	22.3	1325	6	AX213197	AX213197 Sequence
24	154.8	22.3	1325	9	AF246999	AF246999 Homo sapi
25	154.8	22.3	1364	9	AB040434	AB040434 Homo sapi
26	154.8	22.3	1660	6	AX213195	AX213195 Sequence
27	154.8	22.3	1660	6	AF246998	AF246998 Homo sapi
28	151.2	21.8	893	6	AR171888	AR171888 Sequence
29	150.8	21.8	205736	2	AC023560	AC023560 Homo sapi
30	144.2	20.8	43294	2	AC100492	AC100492 Mus muscu
31	132.8	19.2	591	10	AF167554	AF167554 Mus muscu
32	132.8	19.2	623	6	AR171889	AR171889 Sequence
33	120	17.3	190747	2	AC096891	AC096891 Rattus no
34	96	13.9	431	6	AX127571	AX127571 Sequence
35	95.2	13.7	401	6	AX127567	AX127567 Sequence
36	77.4	11.2	190747	2	AC096891	AC096891 Rattus no
37	76	11.0	43294	2	AC100492	AC100492 Mus muscu
38	75.8	10.9	143420	9	AL161422	AL161422 Human DNA
39	51.2	7.4	67259	2	AC100501	AC100501 Mus muscu
40	44.6	6.4	125020	9	AF429315	AF429315 Homo sapi
41	40.2	5.8	1260	10	AF411030	AF411030 Mus muscu
42	40.2	5.8	60709	2	AC107923	AC107923 Homo sapi
43	40.2	5.8	60709	2	AC107923	AC107923 Homo sapi
44	39	5.6	123551	2	AC005809	AC005809 Homo sapi
45	39	5.6	125020	9	AF429315	AF429315 Homo sapi

ALIGNMENTS

RESULT 1
AX127536 1162 bp DNA linear PAT 15-MAY-2001
LOCUS AX127536
DEFINITION Sequence 1 from Patent WO0130850.
ACCESSION AX127536
VERSION AX127536.1 GI:14134241
KEYWORDS
SOURCE
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1162)
AUTHORS Xu,W., Lofton-Day,C.E., Henne,R., Yao,Y., Novak,J.E., Foster,D.C.
and Yee,D.P.
TITLE Umlr polypeptides
JOURNAL Patent: WO 0130850-A 1 03-MAY-2001;
Zymogenetics, Inc. (US)
FEATURES
source location/Qualifiers
1..1162
/organism="Homo sapiens"
/db_xref="taxon:9606"
104..913
/note="unnamed protein product"

Db	421	GCNTTNGTNMSWSMYTTWTGTGTCNTTNTYACANTINGCNTYYTYTGNGAYNTTNTTTTTN	480
Qy	481	TACTGCAGCAGTCTTCCACAGACATTTGCCAGCGTGGAGCTTTGCTCCAGTTTGAGGCT	540
Db	481	TATYTGAARCAATTYYTAAYMGNCATYGYCARBMGNNGNGNYTNTNCARTTYGARGCN	540
Qy	541	CATAAACACGAAGAAGAAATCTCTTCCCCGCTGCCACCAGACAAGAGACCACTGCT	600
Db	541	GAYAARAACNGCNAAGARGAARSNTNTNTTTCGNGTNCNCNMWMAARGARACMWSNCGN	600
Qy	601	GAGTCCAAGTCTTGTGGGCCCCGTCGACGCTTGGCCAGTTGCTCTCTGAGACTGCTT	660
Db	601	GARMSNCARGARMSNTTATCANATGSCNMNSNYGIACMWSNGARMSNCATYMSCATYGGGTN	660
Qy	661	CCTATATACC	668
Db	661	CAYMSNCC	668
RESULT 5			
LOCUS	AX127585	1081 bp	DNA linear PAT 15-MAY-2001
DEFINITION	Sequence 50 from Patent WO0130850.		
ACCESSION	AX127585		
VERSION	AX127585.1 GI:14134277		
KEYWORDS			
SOURCE	' synthetic construct.		
ORGANISM	synthetic construct		
REFERENCE	artificial sequence.		
AUTHORS	Xu W., Lofton-Day, C.E., Henne, R., Yao, Y., Novak, J.E., Foster, D.C. and Yee, D.P.		
TITLE	Umlr polypeptides		
JOURNAL	Patent: WO 0130850-A 50 03-MAY-2001;		
FEATURES	ZymoGenetics, Inc. (US)		
source	Location/Qualifiers		
	1..1081		
BASE COUNT	248 a 311 c 306 g 216 t		
ORIGIN			
Query Match	59.6%;	Score 413.2;	DB 6; Length 1081;
Best Local Similarity	99.3%;	Pred. No. 2.5e-109;	
Matches 415;	Conservative 0;	Mismatches 3;	Indels 0; Gaps 0;
Qy	1	ATGGATTGGCAGAAATAGTAGTCTGGGACCAATGGGAGCGGTGTGTCACCTGCCAACGG	60
Db	1	ATGGATTGGCAGAAATATAGTAGTCTGGGACCAATGGGAGCGGTGTGTCACCTGCCAACGG	60
Qy	61	TGTGTCTCTGACAGAGAGCTATCCAAAGATTTGTATTATGAGAGGGTGGAGTGGCTTAC	120
Db	61	TGTGTGCTCTGACAGAGAGCTATCCAAAGATTTGTATTATGAGAGGGTGGAGTGGCTTAC	120
Qy	121	TGCACACGCTCGCCCTCTCTGCGAGGTACAAACACAGCTGGGGGCCACACAAAATGTAGACT	180
Db	121	TGCACACGCTCGCCCTCTCTGCGAGGTACAAACACAGCTGGGGGCCACACAAAATGTAGACT	180
Qy	181	TGCATCACCTGTGCTGTCTCATCTGTTCAAGAGGTAACTGGACACACTACTCTAAT	240
Db	181	TGCATCACCTGTGCTGTCTCATCTGTTCAAGAGGTAACTGGACACACTACTCTAAT	240
Qy	241	GCTGTCTGTGGGGACTGTTTGGCCAGGTTCTACCGAAGACACAGCATTTGGAGGCTTCAG	300
Db	241	GCTGTCTGTGGGGACTGTTTGGCCAGGTTCTACCGAAGACACAGCATTTGGAGGCTTCAG	300
Qy	301	GACCAAGATGCATCCCTGTGCAAGACAGACCCCACTCTGAGGTTCAAATGTGCTTC	360
Db	301	GACCAAGATGCATCCCTGTGCAAGACAGACCCCACTCTGAGGTTCAAATGTGCTTC	360
Qy	361	CAGTTGAGTTATGTGAGGACAGTGTGACCCACAGTCCCTCAGAGGCCCACACTGTG	418
Db	361	CAGTTGAGTTATGTGAGGACAGTGTGACCCACAGTCCCTCAGAGGCCCACACTGTG	418

DB	361	CAGTTGAGCTTAGTGTGGAGGCAATGACACCAAGTGGCCCGCTCAGAGAGTACCGCTTG	418
RESULT 6	AX127556	534 bp	Linear
LOCUS	AX127556		
DEFINITION	Sequence 21 from Patent W00130850.		
ACCESSION	AX127556		
VERSION	AX127556.1	GI:14134254	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS	Xu,W., Lofton-Day,C.E., Henne,R., Yao,Y., Novak,J.E., Foster,D.C. and Yee,D.P.		
TITLE	Umlr polypeptides		
JOURNAL	Patent: WO 0130850-A 21 03-MAY-2001;		
FEATURES			
source	1..534	Location/Qualifiers	
BASE COUNT	125 a 136 c 155 g 118 t		
ORIGIN			
Query Match	56.7%;	Score 393.2;	DB 6; length 534;
Best Local Similarity	99.2%;	Pred. No. 1.6e-103;	
Matches	395; Conservative	0; Mismatches	3; Indels 0; Gaps 0;
QY	4	GATGGCCAGAAATATGATGCTGAGCAATGAGGAGCGGTGTGCACCTGCACACGGTGT	63
DB	109	GATGGCCAGAAATATGATGCTGAGCAATGAGGAGCGGTGTGCACCTGCACACGGTGT	168
QY	64	GGTCTGAGCAGAGAGCTATCCAAGATTGTGTTATGAGAGGGTGGAGATGCTTACTGC	123
DB	169	GGTCTGAGCAGAGAGAGCTATCCAAGATTGTGTTATGAGAGGGTGGAGATGCTTACTGC	228
QY	124	ACAGCCTCGCCCTCTCTGCGAGGTACAAAGACAGCTGGGGCCACACAAATGTAGAGTTGC	183
DB	229	ACAGCCTCGCCCTCTCTGCGAGGTACAAAGACAGCTGGGGCCACACAAATGTAGAGTTGC	288
QY	184	ATACCTGTCGTCTCATATGCTTTCAGAGGTCAATGTCACAGCTTCTATGCT	243
DB	289	ATACCTGTCGTCTCATATGCTTTCAGAGGTCAATGTCACAGCTTCTATGCT	348
QY	244	GTCGTGGGGACTGTTTGGCCAGGTTCTACCGAAGACACGCAATTGGAGGCTGCAGGAC	303
DB	349	GTCGTGGGGACTGTTTGGCCAGGTTCTACCGAAGACACGCAATTGGAGGCTGCAGGAC	408
QY	304	CAGAATGATCCCGTGCAGAAAGACACCCCACTCTGAGGTTCAATGTGCTTCCAG	363
DB	409	CAGAATGATCCCGTGCAGAAAGACACCCCACTCTGAGGTTCAATGTGCTTCCAG	468
QY	364	TTGAGCTTAGTGGAGGCAATGACACCAAGTGGCC 401	
DB	469	TTGAGCTTAGTGGAGGCAATGACACCAAGTGGAGCC 506	
RESULT 7	AX127557	1200 bp	DNA
LOCUS	AX127557		
DEFINITION	Sequence 22 from Patent W00130850.		
ACCESSION	AX127557		
VERSION	AX127557.1	GI:14134255	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS	Xu,W., Lofton-Day,C.E., Henne,R., Yao,Y., Novak,J.E., Foster,D.C. and Yee,D.P.		
TITLE	Umlr polypeptides		

JOURNAL	Patent: WO 0130850-A 22 03-MAY-2001;			
FEATURES	ZymoGenetics, Inc. (US)	Location/Qualifiers		
Source	1. .800 /organism="synthetic construct" /db_xref="taxon:32630" /note="construct"			
BASE COUNT	290 a	358 c	330 g	222 t
ORIGIN				
Query Match	56.7%;	Score 393.2;	DB 6;	Length 1200;
Best Local Similarity	99.2%;	Pred. No. 1.7e-103;		
Matches 395;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
OY	4	GATTGCCAAGAAATGACTGCTGGACCAATGGGACGGTGTGTCACTGCCAACGGTGT	63	
Db	109	GATTTCCCAAGAAAAAGATGACTGCGACCAATGGGACGGTGTGTCACTGCCAACGGTGT	168	
OY	64	GGTCTGACAGACGACTATCCAAAGATTGTGTATMGAGAGGGTGGAGATGCCATCTGC	123	
Db	169	GGTCTGTGACAGAGACCTATCCAAAGATTGTGTATMGAGAGGGTGGAGATGCCATCTGC	228	
OY	124	ACAGCCTGCCCTCCTCCGACAGGTACAAAAGACACCTGGGGCCACACAAATGTGAGATTGC	183	
Db	229	ACAGCCTGCCCTCCTCCGACAGGTACAAAAGACACCTGGGGCCACACAAATGTGAGATTGC	288	
OY	184	ATCACCTGTGCTGTATCAATGTGTGTTCAGAAAGGTCACTGCACAGCTTAACTTAACTGT	243	
Db	289	ATCACCTGTGCTGTATCAATGTGTGTTCAGAAAGGTCACTGCACAGCTTAACTTAACTGT	348	
OY	244	GTCTGTGGGGACTGTTTGTCCCGAGTTTCTAACCAAAAGACACGCAATTGGAGAGCCTGGAGAGAC	303	
Db	349	GTCTGTGGGGACTGTTTGTCCCGAGTTTCTAACCAAAAGACACGCAATTGGAGAGCCTGGAGAGAC	408	
OY	304	CAAGAGTGCATCCGTGTCACAGACGACACCCACCTGTGAGTTCAATGTGCTTCCAG	363	
Db	409	CAAGAGTGCATCCGTGTCACAGACGACACCCACCTGTGAGTTCAATGTGCTTCCAG	468	
OY	364	TTGACCTTAGTGGAGGACGATGACCCACAGTGGCCCCC	401	
Db	469	TTGACCTTAGTGGAGGACGATGACCCACAGTGGAGCC	506	
RESULT 8				
AX127565	AX127565	801 bp	DNA	linear
LOCUS	AX127565	801 bp	DNA	linear
DEFINITION	Sequence 30 from Patent W00130850.			
ACCESSION	AX127565			
VERSION	AX127565.1	GI:14134261		
KEYWORDS	. synthetic construct.			
SOURCE	synthetic construct.			
ORGANISM	artificial sequence.			
REFERENCE	1 (bases 1 to 801)			
AUTHORS	Xu,W., Lofton-Day,C.E., Henne,R., Yao,Y., Novak,J.E., Foster,D.C.			
TITLE	Umlr polypeptides			
JOURNAL	Patent: WO 0130850-A 30 03-MAY-2001;			
FEATURES	ZymoGenetics, Inc. (US)	Location/Qualifiers		
Source	1. .801 /organism="synthetic construct" /db_xref="taxon:32630" /note="degenerate sequence"			
misc_feature	1..801	/note="n = A,T,C or G"		
BASE COUNT	132 a	100 c	140 g	88 t
ORIGIN				
Query Match	45.8%;	Score 317.4;	DB 6;	Length 801;
Best Local Similarity	59.6%;	Pred. No. 2e-81;		
Matches 265;	Conservative 0;	Mismatches 83;	Indels 0;	Gaps 0;

[illegible]

[illegible]

RESULT	10
AX127568	
LOCUS	AX127568 528 bp DNA Linear PAT 15-MAY-2001
DEFINITION	Sequence 33 from Patent WO0130850.
ACCESSION	AX127568
VERSION	AX127568.1 GI:14134264
KEYWORDS	.
SOURCE	human.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 528) Xu,W., Lottion-Day,C.E., Henne,R., Yao,Y., Novak,J.E., Foster,D.C. and Yee,D.P. Unlr polypeptides Patent: WO 0130850-A 33 03-MAY-2001; ZymoGenetics, Inc. (US) Location/Qualifiers 1..528 /organism="Homo sapiens" /db_xref="taxon:9606"
TITLE	
REFERENCE	
AUTHORS	
FEATURES	
source	
BASE COUNT	119 a 158 c 135 g 116 t
ORIGIN	

Query Match	37.1%;	Score 257;	DB 6;	Length 528;
Best Local Similarity	97.8%;	Pred. No. 7.5e-64;		
Matches 273;	Conservative	0;	Mismatches 0;	Indels 6;
				Gaps 1.

QY	339	CTCTAGAGGTTCAATATGGCTTCCAGTTGAGCTTAATGAGGAGGAGATGACACCAAGTGGC	398
QY	1	CTCTAGAGGTTCAATATGGCTTCCAGTTGAGCTTAATGAGGAGGAGATGACACCAAGTGGC	60
QY	399	CCCTCAGAGGACACACTTTGTCACCTGCTGAGCAGCCGCTAGTGGTGTAACTCTGAC	458
DB	61	CCCTCAGAGGACACACTTTGTCACCTGCTGAGCAGCCGCTAGTGGTGTAACTCTGAC	120
QY	459	CTTCTCTGGGGCTCTTCTCTCTACTGCAAGCAGTTCTTCAACAGACATTTGCCAGGT--	516
DB	121	CTTCTCTGGGGCTCTTCTCTCTACTGCAAGCAGTTCTTCAACAGACATTTGCCAGGTGT	180
QY	517	----GGAGGTTTGGTCGACGTTTGAGGCTGATTAACAGCAAGCAAGGAGGATTCCTCTGCC	572
DB	181	TGCAGAGAGGTTTGGTCGACGTTTGAGGCTGATTAACAGCAAGCAAGGAGGATTCCTCTGCC	240
QY	573	CGTGCACCCAGCAAGAGAGACCAAGTGTGAGTGTCCCAAGT	611
DB	241	CGTGCACCCAGCAAGAGAGACCAAGTGTGAGTGTCCCAAGT	279

RESULT 11

LOCUS	AX127566				
DEFINITION	AX127566	529 bp		Linear	PAT 15-MAY-2001
ACCESSION	Sequence 31	from Patent WO0130850.			
VERSION	AX127366				
KEYWORDS	AX127566.1	GI:14134262			
SOURCE	.				
ORGANISM	human.				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 529)				
	Xu, W., Lotton-Day, C. E., Henne, R., Yao, Y., Novak, J. E., Foster, D. C.				
	and Yee, D. P.				
TITLE	Umlr polypeptides				
JOURNAL	Patent: WO 0130850-A 31 03-MAY-2001;				
	Zymogenetics, Inc. (US)				
FEATURES	Location/Qualifiers				
source	1..529				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
misc_feature	1..529				
	/note="n = A,T,C or G"				
BASE COUNT	116 a	135 c	126 g	107 t	45 others
ORIGIN					

Query Match	Match Similarity	31.8%	Score 220.4	DB 6	Length 529
Best Local	Similarity 86.0%	Score NO. 3.5e-53			
Matches 240	Conservative 16	Mismatches 21	Indels 2	Gaps 2	
QY	335	CCACCTCTAGTTCATATGCTTCCTCCACTTAACTTAAGCTTAACTGGAGGCACATATGCACCCACAG	394		
Db	6	CNATNNCGAGGNTGATGAGCGMTTCAGATTNNCASTKATGTGAGGCACAGATGCASCACAG	65		
QY	395	TGCCCC-CTCAGAGAGGCACACTTGTGTGCATCGTGAGAGCAGCTGTGTAAGTGTATACC	453		
Db	66	TGCCCGCCCTCAGAGAGGYCACACTTGTGTGCTGATGAGAGCAGCTGTGTAAGTGTATACC	125		
QY	454	CTGGCTTCCTGGGGGCTCTCTTCCTCCATCTGCAGAACCACTTCTTCAACAGCAATTGCCAG	513		
Db	126	CTGGCTTCCTGGGGGCTCTCTTCCTCCATCTGCAGAACCACTTCTTCAACAGCAATTGCCAG	185		
QY	514	C-CTGAGAGTTTGTCTGCACATTTGAGGCTGATAAACAGCAAAAGAGAAATCTCTTCC	572		
Db	186	CSGNGAGAGTTTGTCTGCACATTTGAGGCTGATRAAACAGCAAAAGAGAAATCTSTMTTTCY	245		
QY	573	CGTGCACCCACAGCAGAGAGACCAAGTCCTGAGTCCCAAGT	611		
Db	246	CGTGCACCCACAGCAGAGAGACCAAGTCCTGAGTCCCAAGT	284		

RESULT 12	AL353136/c	AL353136	192505 bp	DNA	linear	PRI 09-MAR-2001
LOCUS						
DEFINITION		Human DNA sequence from clone RPl1-133K18 on chromosome X, complete sequence.				
ACCESSION	AL353136					
VERSION	AL353136.21	GI:13274342				
KEYWORDS	HTG.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.					
AUTHORS	1 (bases 1 to 192505)					
TITLE	Heach, P.					
JOURNAL	Direct Submission					
COMMENT	Submitted (08-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: hunkmeyer@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk					
	On Mar 12, 2001 this sequence version replaced gi:1321368.					
	During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations					
	together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission					

corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWSNPOT; Tr: TRMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/ChrX>
RP11-133K18 is from the library RPC1-11.1 constructed by the group of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>
VECTOR: pBAC3.6

This sequence is the entire insert of clone RP11-133K18 The true left end of clone RP3-4304 is at 146164 in this sequence.

Location/Qualifiers

FEATURES

source

1..192505
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
/clone="RP11-133K18"
/clone_lib="RPC1-11.1"
2..590
/note="match: GSS: Em:A0415618"
8..241
/note="L1M4 repeat: matches 4301..4547 of consensus"
9..465
/note="match: GSS: Em:A2516005"
312..748
/note="L1M2 repeat: matches 5844..6304 of consensus"
864..1686
/note="L1P11 repeat: matches 5308..6165 of consensus"
/note="match: GSS: Em:A0076345"
/note="match: GSS: Em:A0076345"
/note="match: GSS: Em:A0456867"
6871..6916
/note="23 copies 2 mer at 100% conserved"
6947..7069
/note="MER21A repeat: matches 822..927 of consensus"
7070..7365
/note="AluX repeat: matches 1..296 of consensus"
7366..7498
/note="MER21A repeat: matches 684..822 of consensus"
7501..7661
/note="MER21B repeat: matches 363..523 of consensus"
7520..7927
/note="match: GSS: Em:A0021529"
7862..8255
/note="MER21A repeat: matches 3..406 of consensus"
8256..10065
/note="L1M1 repeat: matches -1213..643 of consensus"
10066..11582
/note="L1M1 repeat: matches 895..2792 of consensus"
11574..12563
/note="L1M3 repeat: matches 4976..5378 of consensus"
12538..13476
/note="L1P15 repeat: matches 5171..6055 of consensus"
13477..14163
/note="L1M1 repeat: matches 5616..6299 of consensus"
14164..18546
/note="L1P15 repeat: matches 656..5171 of consensus"
19058..19370
/note="L1P13 repeat: matches -651..-339 of consensus"

repeat_region 19380..19427
/note="L1P13 repeat: matches 6109..6156 of consensus"
repeat_region 20158..20170
/note="L12 repeat: matches 992..1002 of consensus"
repeat_region 20171..20593
/note="MSTB repeat: matches 1..426 of consensus"
repeat_region 20594..20722
/note="L12 repeat: matches 1002..1147 of consensus"
repeat_region 20803..21452
/note="L12 repeat: matches 1635..2587 of consensus"
repeat_region 21924..22023
/note="MIR repeat: matches 4..106 of consensus"
repeat_region 23030..23050
/note="L1P4 repeat: matches 5372..5391 of consensus"
repeat_region 23051..23600
/note="L1P13 repeat: matches 5596..6156 of consensus"
repeat_region 23601..24341
/note="L1P4 repeat: matches 4790..5372 of consensus"
misc_feature complement(24172..24658)
/note="match: GSS: Em:A0617974"
25450..27192
/note="L1P12 repeat: matches 4389..6155 of consensus"
repeat_region 27175..28098
/note="L1P11 repeat: matches 3245..4193 of consensus"
repeat_region 28098..28541
/note="L1 repeat: matches 2176..2620 of consensus"
repeat_region 28544..29065
/note="L1P4 repeat: matches 5626..6146 of consensus"
repeat_region 29066..29291
/note="L1P4 repeat: matches 5398..5626 of consensus"
repeat_region 29281..29770
/note="L1M2 repeat: matches 1623..2196 of consensus"
repeat_region 29774..29945
/note="AluSg/x repeat: matches 134..305 of consensus"
repeat_region 29957..32877
/note="L1P11 repeat: matches 2930..5805 of consensus"
repeat_region 32882..33025
/note="72 copies 2 mer ta 66% conserved"
repeat_region 33027..33390
/note="L1P11 repeat: matches 5781..6155 of consensus"
repeat_region 33538..35294
/note="L1M3A repeat: matches 501..1804 of consensus"
repeat_region 35271..35571
/note="L1M3A repeat: matches 745..904 of consensus"
repeat_region 35778..36216
/note="L1M3A repeat: matches 213..655 of consensus"
repeat_region 36287..36471
/note="MIR repeat: matches 57..251 of consensus"
repeat_region 36769..37123
/note="L1M1 repeat: matches 5597..5884 of consensus"
repeat_region 37140..38332
/note="L1M3 repeat: matches 5105..6299 of consensus"
repeat_region 38339..38440
/note="L1 repeat: matches 2434..2535 of consensus"
repeat_region 38446..38807
/note="MUT2B repeat: matches 1..374 of consensus"
repeat_region 38879..39795
/note="HEBV repeat: matches 1..916 of consensus"
repeat_region 39796..40402
/note="L1P2 repeat: matches 5050..5656 of consensus"
repeat_region 40403..40850
/note="L1P4 repeat: matches 5639..6146 of consensus"
repeat_region 40890..45577
/note="HEBV repeat: matches 905..5578 of consensus"
repeat_region 45578..45888
/note="AluX repeat: matches 1..311 of consensus"
repeat_region 45889..45965
/note="HEBV repeat: matches 5578..5654 of consensus"
repeat_region 45966..46346
/note="MUT2B repeat: matches 1..392 of consensus"
repeat_region 46451..49891
/note="L1M1 repeat: matches -1390..2500 of consensus"
repeat_region 49928..50810

```

repeat_region /note="L1M4 repeat: matches 3343. .4258 of consensus"
50989. .51126 /note="69 copies 2 mer tt 59% conserved"
repeat_region 51129. .51365
/note="L1P4 repeat: matches 5910. .6146 of consensus"
repeat_region 51367. .52126
/note="L1P2 repeat: matches 4727. .5487 of consensus"
repeat_region 52758. .53940
/note="L1 repeat: matches 4150. .5350 of consensus"
repeat_region 53994. .54310
/note="L1M5 repeat: matches 7581. .7917 of consensus"
repeat_region 54357. .54551
/note="L1P3 repeat: matches 5847. .6127 of consensus"
repeat_region 54560. .54862
/note="Aluv repeat: matches 1. .303 of consensus"
repeat_region 55116. .57271
/note="L1P8 repeat: matches 3978. .6163 of consensus"
repeat_region 57372. .57301
/note="L1P4 repeat: matches 5338. .5367 of consensus"
repeat_region 57302. .57608
/note="AlusX repeat: matches 1. .306 of consensus"
repeat_region 57609. .57770
/note="L1P4 repeat: matches 5367. .5525 of consensus"
repeat_region 57747. .64039
/note="L1P7 repeat: matches 6. .5917 of consensus"
repeat_region 64050. .64157
/note="54 copies 2 mer at 90% conserved"
repeat_region 64162. .65850
/note="L1P2 repeat: matches 4456. .6146 of consensus"
repeat_region 65847. .66663
/note="L1P2 repeat: matches 3623. .4439 of consensus"
repeat_region 66640. .66882
/note="L1P7 repeat: matches 5894. .6134 of consensus"

```

```

Query Match 26.2%; Score 181.4; DB 9; Length 192505;
Best Local Similarity 99.5%; Pred. No. 1.2e-41;
Matches 182; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 86 AGGATTGGCTTATGAGAGGCTGAGATGCTCTGACAGCCCTGCTGCGCAGCT 145
|||||
Db 109481 AGGATTGGCTTATGAGAGGCTGAGATGCTCTGACAGCCCTGCTGCGCAGCT 109422

QY 146 ACAAAAGCAGCTGGGGCCACCAATGTGAGATTGCATCAGCTGCTGCATCAATC 205
|||||
Db 109421 ACAAAAGCAGCTGGGGCCACCAAGATGTCAGATTGCATCAGCTGCTGCATCAATC 109362

QY 206 GTGTTCAAGAGTCACTGCACAGCTACCTCTAATGCTGTGTGGGAGCTGTTGCCCA 265
|||||
Db 109361 GTGTTCAAGAGTCACTGCACAGCTACCTCTAATGCTGTGTGGGAGCTGTTGCCCA 109302

QY 266 GGT 268
|||
Db 109301 GGT 109299

```

```

RESULT 13
AC023560/c 205736 bp DNA linear HTG 12-MAR-2000
LOCUS Homo sapiens chromosome 17 clone RP11-85120 map 17, WORKING DRAFT
DEFINITION AC023560
SEQUENCE, 34 unordered pieces.
ACCESSION AC023560
VERSION AC023560.2 GI:7222913
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 205736)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 17, clone RP11-85120
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 205736)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,

```

TITLE JOURNAL COMMENT

Anderson,S., Baldwin,J., Barna,N., Beda,F., Boguslavsky,L.,
Boukhalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
Choepl,Y., Collangelo,M., Collins,S., Collymore,A., Cooke,P.,
DeRellano,K., Dewar,K., Dodge,S., Domino,M., Doyle,M.,
Fenster,J., Ferreira,P., FitzHugh,W., Forrest,C., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., Landers,T., Laroque,K., Lebecky,J., Levine,R.,
Lieu,C., Liu,G., Locke,K., MacDonald,P., Margis,N., McCarthy,M.,
McMan,P., McGuck,A., McKernan,K., McPheters,R., Meldrum,D.,
Meneus,L., Mihova,T., Miranda,C., Mienna,V., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,T.M.,
Peterson,K., Pierre,N., Pisanl,C., Pollara,V., Raymond,C.,
Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S.,
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Subramanian,A., Talamas,J., Testaye,S., Theodore,J., Tirell,A.,
Travers,M., Triggillo,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B.,
Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and
Zody,M.

Direct Submission
Submitted (15-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 12, 2000 this sequence version replaced gi:6978256.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www.seq.wi.mit.edu>
Contact: sequence.submissions@genome.wi.mit.edu

Project Information

Center project name: 16741
Center clone name: 85_1-20

Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 17866 bases at least Q40
Consensus quality: 190940 bases at least Q30
Consensus quality: 197088 bases at least Q20
Insert size: 19400; agarose-fp
Insert size: 202436; sum-of-contigs
Quality coverage: 4.2 in Q20 bases; agarose-fp
Quality coverage: 4.0 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently
consists of 34 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

1 1267: contig of 1267 bp in length
* 1268 1367: gap of 100 bp
* 1368 2402: contig of 1035 bp in length
* 2403 2502: gap of 100 bp
* 2503 3524: contig of 1022 bp in length
* 3525 3624: gap of 100 bp
* 3625 4913: contig of 1289 bp in length
* 4914 5013: gap of 100 bp
* 5014 6289: contig of 1276 bp in length
* 6290 6389: gap of 100 bp
* 6390 7655: contig of 1266 bp in length
* 7656 7755: gap of 100 bp
* 7756 9267: contig of 1512 bp in length
* 9268 9367: gap of 100 bp
* 9368 11138: contig of 1771 bp in length
* 11139 11238: gap of 100 bp
* 11239 13822: contig of 2584 bp in length
* 13823 13922: gap of 100 bp


```
* 13923 16968: contig of 3046 bp in length
* 16969 17068: gap of 100 bp
* 17069 20185: contig of 3117 bp in length
* 20186 20285: gap of 100 bp
* 20286 22634: contig of 2349 bp in length
* 22635 22734: gap of 100 bp
* 22735 27012: contig of 4278 bp in length
* 27013 27112: gap of 100 bp
* 27113 29342: contig of 2230 bp in length
* 29343 29442: gap of 100 bp
* 29443 33381: contig of 3939 bp in length
* 33382 33481: gap of 100 bp
* 33482 36562: contig of 3081 bp in length
* 36563 36662: gap of 100 bp
* 36663 40982: contig of 4320 bp in length
* 40983 41082: gap of 100 bp
* 41083 45520: contig of 4438 bp in length
* 45521 45620: gap of 100 bp
* 45621 50623: contig of 5003 bp in length
* 50624 50723: gap of 100 bp
* 50724 55610: contig of 4887 bp in length
* 55611 55710: gap of 100 bp
* 55711 61038: contig of 5328 bp in length
* 61039 61138: gap of 100 bp
* 61139 66159: contig of 5021 bp in length
* 66160 66259: gap of 100 bp
* 66260 73479: contig of 7220 bp in length
* 73480 73579: gap of 100 bp
* 73580 80554: contig of 6975 bp in length
* 80555 80654: gap of 100 bp
* 80655 89313: contig of 8659 bp in length
* 89314 89413: gap of 100 bp
* 89414 98132: contig of 8719 bp in length
* 98133 98232: gap of 100 bp
* 98233 107469: contig of 9237 bp in length
* 107470 107569: gap of 100 bp
* 107570 117873: contig of 10304 bp in length
* 117874 117973: gap of 100 bp
* 117974 130973: contig of 13000 bp in length
* 130974 131073: gap of 100 bp
* 131074 143236: contig of 12163 bp in length
* 143237 143336: gap of 100 bp
* 143337 154478: contig of 11142 bp in length
* 154479 154578: gap of 100 bp
* 154579 169967: contig of 15389 bp in length
* 169968 170067: gap of 100 bp
* 170068 187347: contig of 17280 bp in length
* 187348 187447: gap of 100 bp
* 187448 205736: contig of 18289 bp in length.
Location/Qualifiers
1. 205736
```

FEATURES

source

```
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
/map="17"
/clone="RP11-85120"
/clone_lib="RP11-85120 Human Male BAC"
1. 1267
misc_feature
/note="assembly_fragment"
1368. 2402
misc_feature
/note="assembly_fragment"
2503. 3524
misc_feature
/note="assembly_fragment"
3625. 4913
misc_feature
/note="assembly_fragment"
5014. 6289
misc_feature
/note="assembly_fragment"
6390. 7655
misc_feature
/note="assembly_fragment"
7756. 9267
misc_feature
/note="assembly_fragment"
9368. 11138
misc_feature
/note="assembly_fragment"
```

```
misc_feature 11239. 13822
/note="assembly_fragment"
misc_feature 13923. 16968
/note="assembly_fragment"
misc_feature 17069. 20185
/note="assembly_fragment"
misc_feature 20286. 22634
/note="assembly_fragment"
misc_feature 22735. 27012
/note="assembly_fragment"
misc_feature 27113. 29342
/note="assembly_fragment"
misc_feature 29443. 33381
vector_side:right
29443. 33381
/note="assembly_fragment"
33482. 36562
/note="assembly_fragment"
36663. 40982
/note="assembly_fragment"
41083. 45520
/note="assembly_fragment"
45621. 50623
/note="assembly_fragment"
50724. 55610
/note="assembly_fragment"
55711. 61038
/note="assembly_fragment"
61139. 66159
/note="assembly_fragment"
66260. 73479
/note="assembly_fragment"
73580. 80554
/note="assembly_fragment"
80655. 89313
/note="assembly_fragment"
89414. 98132
/note="assembly_fragment"
```

Query Match

Best Local Similarity 99.5%; Pred. No. 1,2e-41;

Matches 182; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 86 AGGATTGCTGTATGAGAGGCTGGAGATGCTCTACGACAGCTGCCCTCTCCGACGT 145
|||||
Db 79395 AGGATTGCTGTATGAGAGGCTGGAGATGCTCTACGACAGCTGCCCTCTCCGACGT 79336

QY 146 ACAAAAGCAGCTGGGGCCACACAAATGTCAGAGTTGCATCAGCTGCTGTCATCAATC 205
|||||
Db 79335 ACAAAAGCAGCTGGGGCCACACAGATGTCAGAGTTGCATCAGCTGCTGTCATCAATC 79276

QY 206 GTGTTGGAAGGTCACGACAGCTACCTTAATGCTGCTGTTGGGAGCTGTTGCCCA 265
|||||
Db 79275 GTGTTGGAAGGTCACGACAGCTACCTTAATGCTGCTGTTGGGAGCTGTTGCCCA 79216

QY 266 GGT 268
|||
Db 79215 GGT 79213
```

RESULT 14

AB040433

LOCUS AB040433 744 bp mRNA linear ROD 22-JUL-2000

DEFINITION Mus musculus mRNA for dtroy, complete cds.

AB040433

AB040433.1 GI:9392327

KEYWORDS dtroy.

SOURCE Mus musculus CDNA to mRNA.

ORGANISM Mus musculus

REFERENCE 1 (sites)
AUTHORS Kojima,T., Morikawa,Y., Copeland,N.G., Gilbert,D.J., Jenkins,N.A.,

Senba, E. and Kitamura, T.
TRFY, a newly identified member of the tumor necrosis factor
receptor superfamily, exhibits a homology with Eder and is
expressed in embryonic skin and hair follicles
J. Biol. Chem. 275 (27), 20742-20747 (2000)
DOI: 10.1006/jbc.20003257

Db 643 TGC AAGAGG CAGT TCA 658

RESULT 15
AF167553

FEATURES	
JOURNAL	1 (bases 1 to 886)
PUBMED	Edy,M.T., Jasmin,A., Kumar,A., Sharma,K. and Chaudhary,P.M.
REFERENCE	TAJ, a Novel Member of the Tumor Necrosis Factor Receptor Family,
AUTHORS	Activates the c-Jun N-terminal Kinase Pathway and Mediates
TITLE	Caspase-independent Cell Death
JOURNAL	J. Biol. Chem. 275 (20), 15336-15342 (2000)
PUBMED	10809768
REFERENCE	2 (bases 1 to 886)
AUTHORS	Chaudhary,P.M.
TITLE	Direct Submission
JOURNAL	Submitted (12-JUL-1999) Internal Medicine, UT Southwestern Medical
FEATURES	Center, 5333 Harry Hines Blvd., Dallas, TX 75235-8593, USA
	Location/Qualifiers

```

/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="Soares p3NMF19.5"
72. .716
CDS

```

ORIGIN	BASE COUNT	162 a	208 c	211 g	163 t
Query Match	23.5%;				
Best Local Similarity	58.1%;				
Matches 288; Conservative	0;				
	Pred. No. 1.7e-36;				
	Mismatches 208;				
	Indels 0;				
	Gaps 0;				
QY	4	GATTGCCAAGAAATAGAGTACGTGGGACCAATGGGAGACGGTGTGTACCTGCCAAGGGTGT	63		
Db	163	GATTCCAGGCAAGCAAGAAATTCAGGATGATCTGGAACCTGTCTCTGCACAAAGTGC	222		
QY	64	GGTCTTGACAGAGACTATCCAGAGATTGTGGTATGGAGAGGTGGAGATGCTACTGC	123		
Db	223	GGACCTGGCAGTAGATTGTCCAGGAATGTGGCTTGGCTATGGGAGAGATCCACAGTGT	282		
QY	124	ACAGCTTCGCTCTCTCGCAGGTACAAAGACAGCTGGGGCCACCACAAATGTGAGATTGC	183		
Db	283	GTGCCCTCAGGAGCCGACCGGTTCAAGGAAGACTGGGGTTCCAAAGTGTAAAGCATGT	342		
QY	184	ATCACCTTGCTGTATCATGTGTTCAGAAAGTGCACACTGCACAGTCACTTAATCT	243		
Db	343	GGGACCTGTGGCGTGTGTAAACCGCTTTGAGAGGGCAACTGTCTACACACAGTATCTT	402		
QY	244	GTCGTGGGGAAGCTGTTGCCAGGTTCTACCGAAAGACAGCATGGAGGCTCGCAGAC	303		
Db	403	GTCCTGGGGAAGTGCCTCCAGGATTTACCGGAAGCAACAACTGTTGGTTTCAACAC	462		
QY	304	CAGAAGTCAATCCGTGTCACAGACAGACCCCACTCTGAGGTTCAATGTGCTTCAG	363		
Db	463	ATGGAGTGTGTCCCTGGGAGACCCACCTCCCTCCAGAACCACTGTACACGACAG	522		
QY	364	TTGAGCTAAGTAGGAGGACAGATGACCCCAAGTGGCCCCCTCAGAGAGCCACACTTGTGCA	423		
Db	523	GTTGAACCTTTGAGAAATCTCTCCACACGGTCTTCACCAAGCTTGGGAGACGGCCCTGGCTCC	582		
QY	424	CTGTGAGACAGACTGCTAATGATGTTATCCCTTGAGCCCTCTGGGGCTTTCTTCCTAC	483		
Db	583	GTCATCTGCAAGTGTGCTGGCAAGGTGTGTGGCCCTGCTCATCTGTGTATCTAC	642		
QY	484	TGCAAGCAGTTCTTCA	499		

	BASE COUNT	204 a	245 c	247 g	190 t
Query Match	23.5%	Score 163.2;	DB 10;	Length 886;	
Best Local Similarity	58.1%	Pred. No. 1,7e-36;			
Matches 288;	Conservative	0;	Mismatches 208;	Indels	0; Gaps
0;					
0Y	4	GATGGCCAGAAAMVAGTACTGGGACCAAGGGGAGCGTGTCACCTGGCAGCGGT	63		
Db	168	GATTGCAGGCGACGAGGAATTCAGAGATCGATCGTGAACACTGTGCTTGGAAACAGTGC	227		
0Y	64	GTCCTGGACAGAGACTATCCAGAGATTGGTTATGAGAGAGGGTGGAGATGCCCTACTGC	123		
Db	228	GGACTGGCAGAGAGTGTCCAAAGAAATGTTGGCTTGTGGGAGAGATGCACAGTGT	287		
0Y	124	ACAGCTTGCCTCTCTCGCAGGTACAAAAGCAGCTGGGGCCACCAANAATGTACAGATTGC	183		
Db	288	GTCGCTGCGACGGCGCGACCGGTTCCAAAGAAAGACTGGGGGTTCCGGAAGTGTAAACCATGT	347		
0Y	184	ATCACCTGTGTCATCATATCGTGTTCAGAAAGTTCAAAGTCACAGCTACCTCTAATGCT	243		
Db	348	CGCGACTGTGCTGCTGTGAACCGCTTTCAGAGGGCCAACTCTCACACACCGATGATGCT	407		
0Y	244	GTCGTGGGAGCTGTTTGCCAGGTTTCTACGGAAGAACAGCATTTGAGGGCTTCAGAGAC	303		
Db	408	GTCGGGGGAGCTGCTGCGCCAGGATTTTACCGGAAGCAACATGTTGTTTTCAGAGAC	467		
0Y	304	CAAGATGTATCCGTGTCACGAAGACAGACCCCACTCTGAGGTTCAATGTGCTTCCAG	363		
Db	468	ATGAGAGTGTGCTGCTGGGAGACCCACTCTTCTCCATCAAGAACACACTGTACCGAGAG	527		

	BASE COUNT	204 a	245 c	247 g	190 t
Query Match	23.5%	Score 163.2;	DB 10;	Length 886;	
Best Local Similarity	58.1%	Pred. No. 1,7e-36;			
Matches 288;	Conservative	0;	Mismatches 208;	Indels	0; Gaps
0;					
0Y	4	GATGGCCAGAAAMVAGTACTGGGACCAAGGGGAGCGGTGTGCACCTGGCAGCGGT	63		
Db	168	GATTGCAGGCGAGCGAGGATTCAGAGATCGATCTGGAACACTGTGTCTTGGAACAGTGC	227		
0Y	64	GTCCTGGACAGAGACTATCCAGAGATTGTGTATGAGAGGGGTGAGATGCTTACTGC	123		
Db	228	GGACTGGCAGAGAGTGTCCAAAGAAATGTGGCTTGCGCTATGGGAGAGATGCACAGTGT	287		
0Y	124	ACAGCTTGCCTCTCTGCAGGTACAAAAGCAGCTGGGGCCACCAANAATGTACAGATTGC	183		
Db	288	GTCGCTGCGAGGCGCGACCGGTTCCAAAGAAAGACTGGGGGTTCCGAAGTGTAAACCATGT	347		
0Y	184	ATCACCTGTGTCATCATCTGTTTCAGAAAGTTCAAAGTCACAGCTACCTCTAATGCT	243		
Db	348	CGCGACTGTGCTGCTGTGAACCGCTTTCAGAGGGCCAACTCTCACACACCGATGATGCT	407		
0Y	244	GTCGTGGGAGCTGTTTGCCAGGTTTCTACGGAAGAACAGCATTTGAGGCTTCAGAGAC	303		
Db	408	GTCGGGGGAGCTGCTGCGCCAGGATTTTACCGGAAGCAACATGTTGTGTTTCAAGAC	467		
0Y	304	CAAGATGTATCCGTGCACGAAGACAGACCCCACTCTGAGGTTCAATGTGCTTCAG	363		
Db	468	ATGAGATGTGTGCTGCGGAGAGACCCACTCTCTCCCTACGAACACACTGATACGACAG	527		

THIS PAGE BLANK (USPTO)